

Supplementary material: Global transcriptional programs in archaea share features with the eukaryotic environmental stress response

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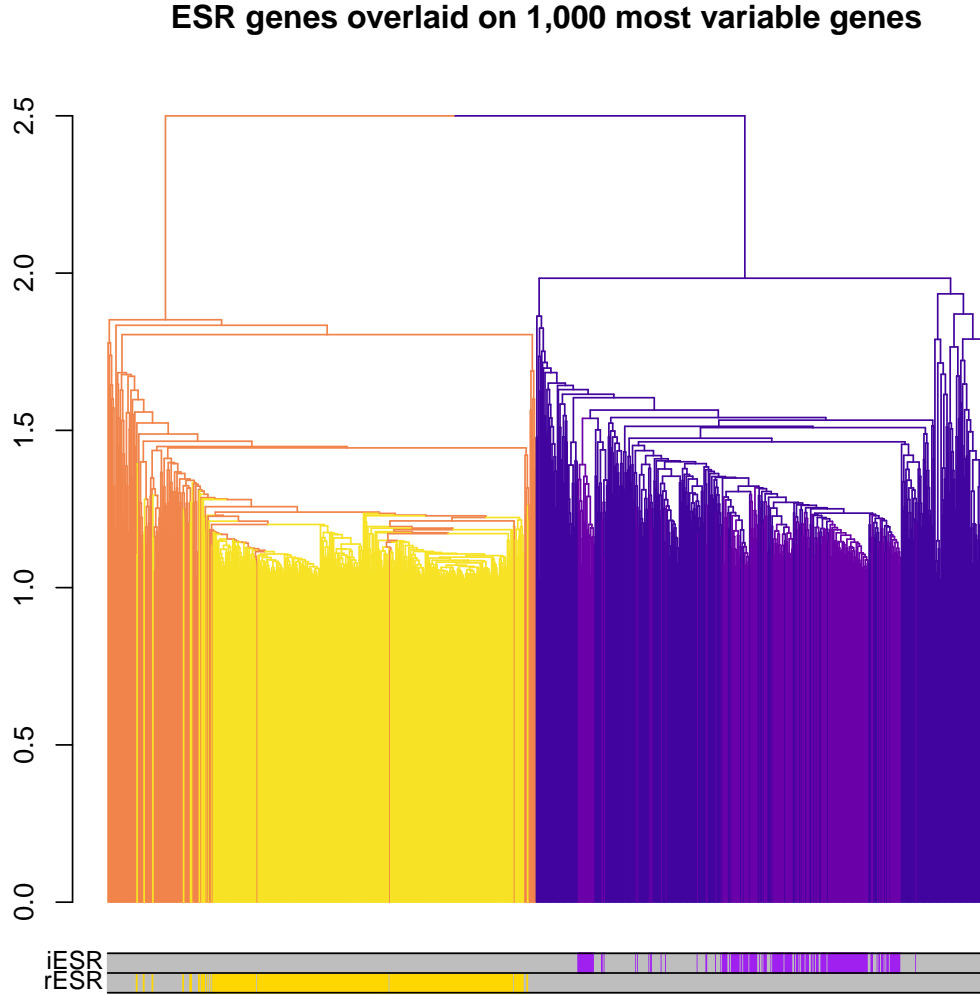


Figure 1: **rESR and iESR clustering is preserved in our filtering strategy.** Dendrogram of 1000 most variable *S. cerevisiae* genes included in manuscript, colored by cluster. Repressed genes are colored in shades of orange and induced genes are colored in shades of purple. The 570 ESR genes that were recapitulated in our analysis are colored in lighter shades in the dendrogram, and also in the rug plot at the termini of the dendrogram leaves. rESR genes originally identified by Gasch et al were also detected within the repressed cluster by our analysis, and original iESR genes were detected in the induced cluster. Hierarchical clustering was performed using Spearman gene correlations, average linkage. Dendrogram was generated using the dendextend package.

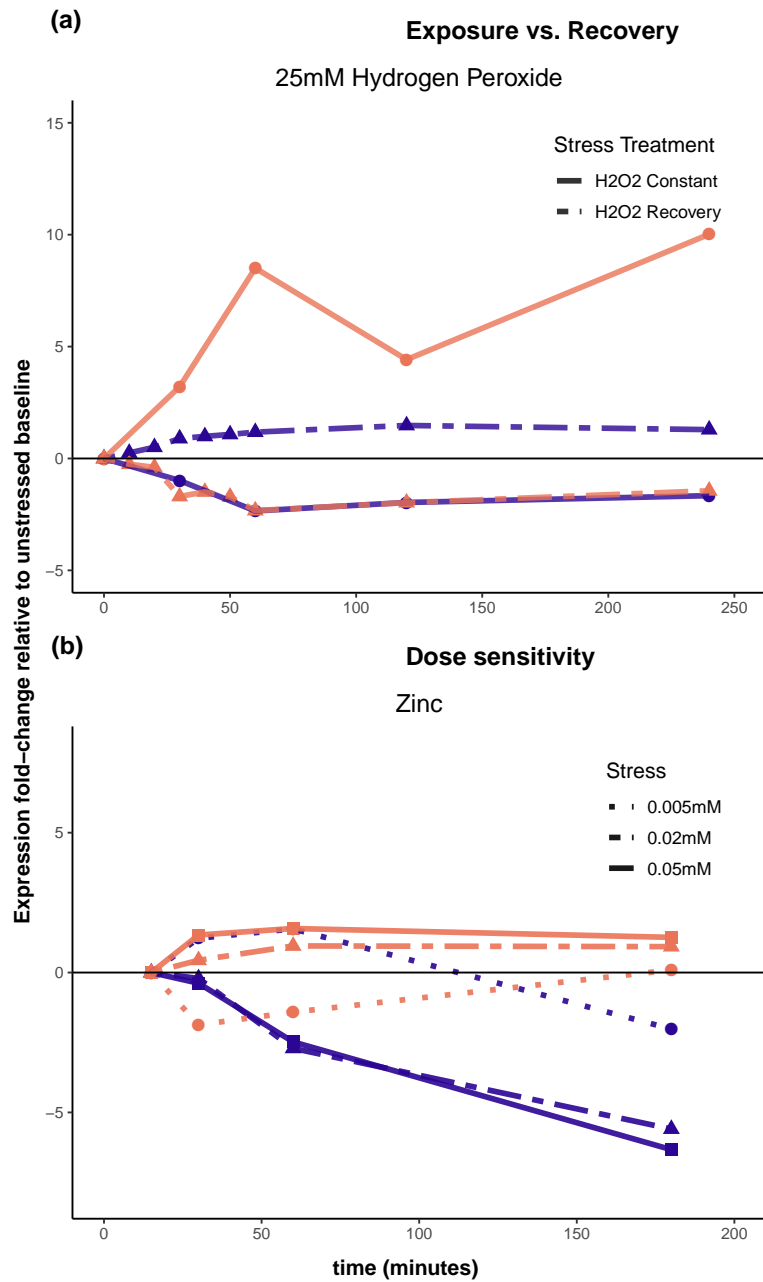


Figure 2: **ESR-like dynamics in *Hbt. salinarum* are not specific to paraquat treatment.** Treatment of high concentrations of hydrogen peroxide induces expression of iESR-like genes (yellow, solid lines), while removal from stressful peroxide conditions stimulates recovery to a nearly un-shocked expression profile (purple and yellow, dashed). (B) Dose responsive dynamics are observed in response to zinc. Average expression induced genes (yellow) and repressed genes (purple) exhibits larger magnitude change at high concentrations (solid) vs lower concentrations (see legend).

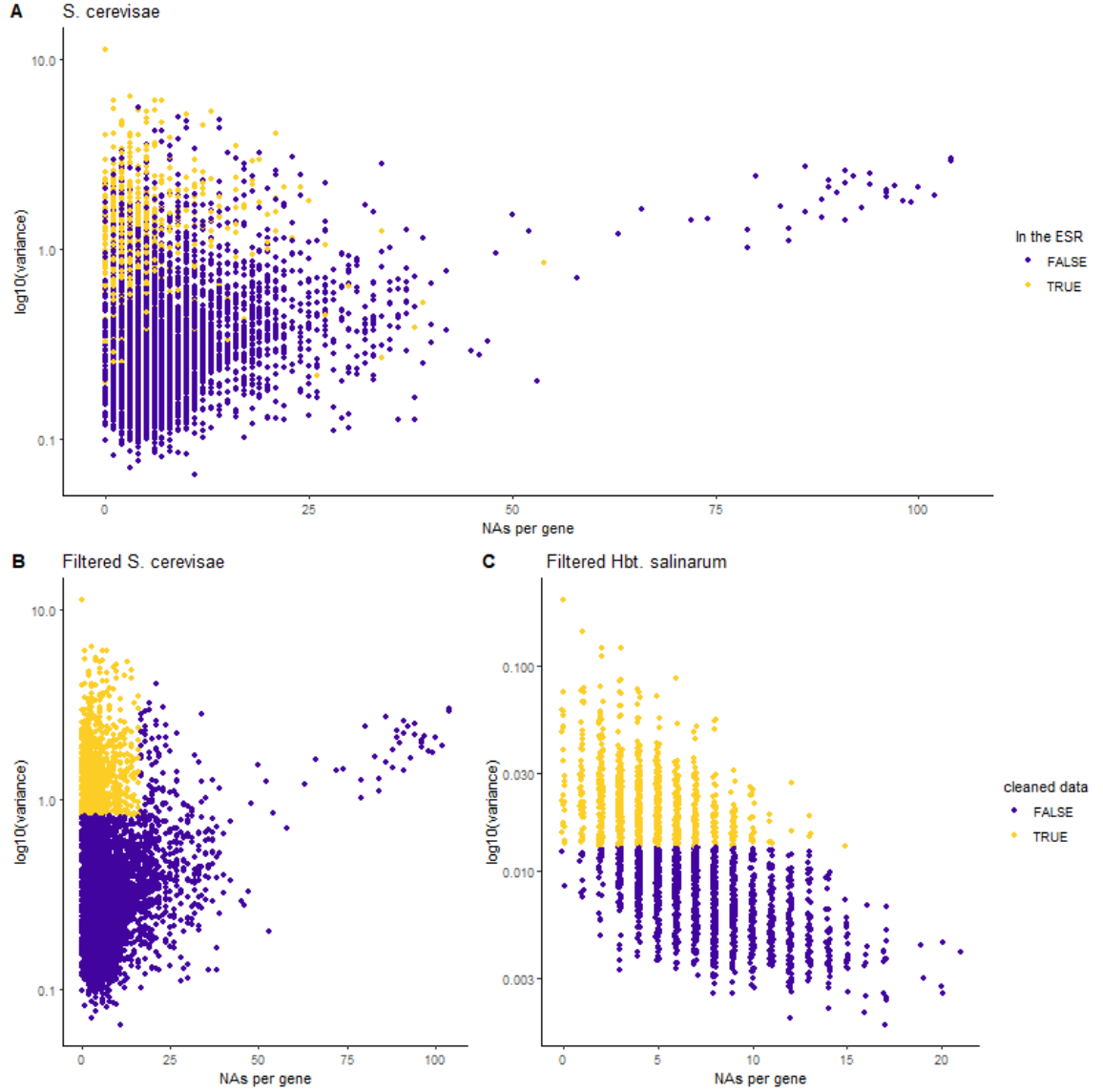


Figure 3: Filtering strategy for selection of 1,000 most variable genes. This figure depicts our filtering strategy of removing genes whose expression was not measured in more than 10% of conditions, and whose expression was highly variable. (A) illustrates the identity of ESR genes (yellow) compared to the *S. cerevisiae* genome (purple). Number of missing values (x-axis) are plotted against log10 variance in gene expression (y-axis). (B) *S. cerevisiae* genes used in the analysis presented in this paper. (C) All *Hbt. salinarum* genes passed the missing value cutoff, and genes presented in our analysis are represented in yellow. Note the greater overall variance for *S. cerevisiae* data is in part due to the time-zero transformation that was used for time-series measurements within conditions.